

FIG. 1A

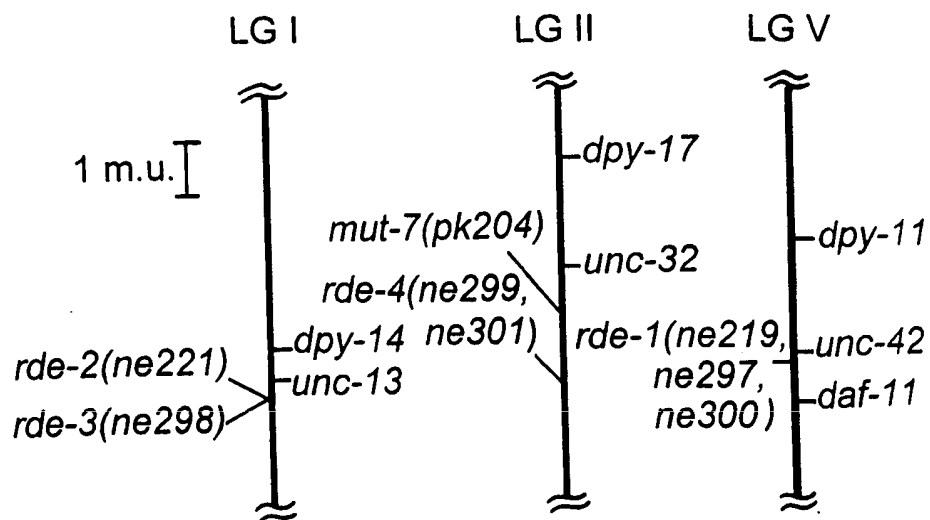
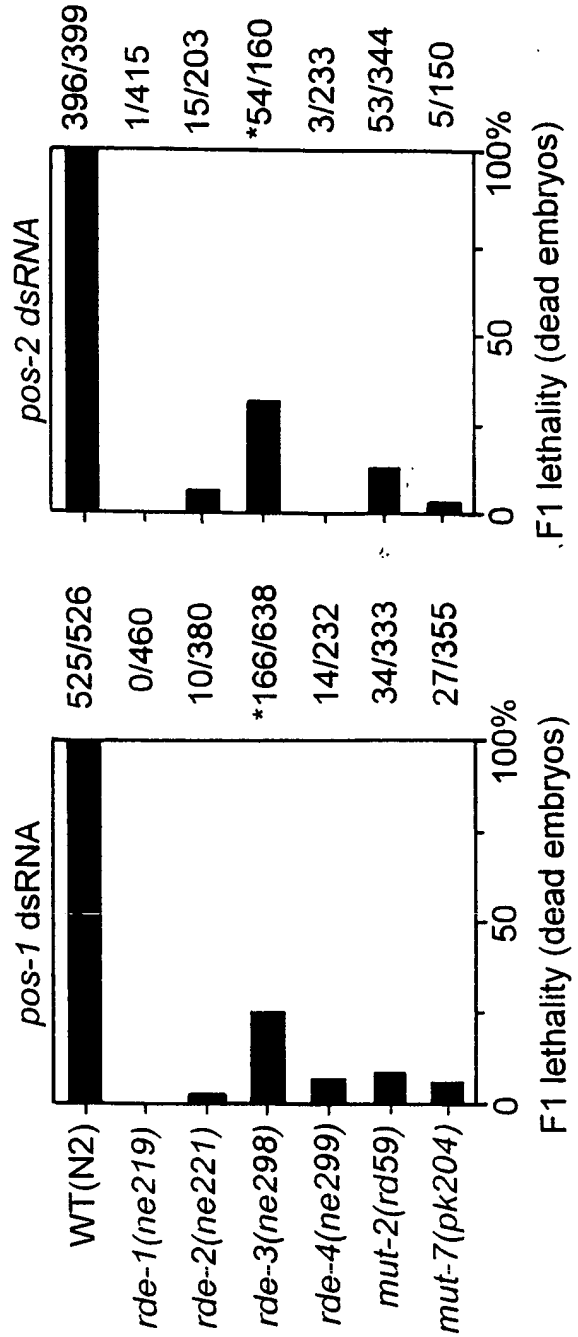
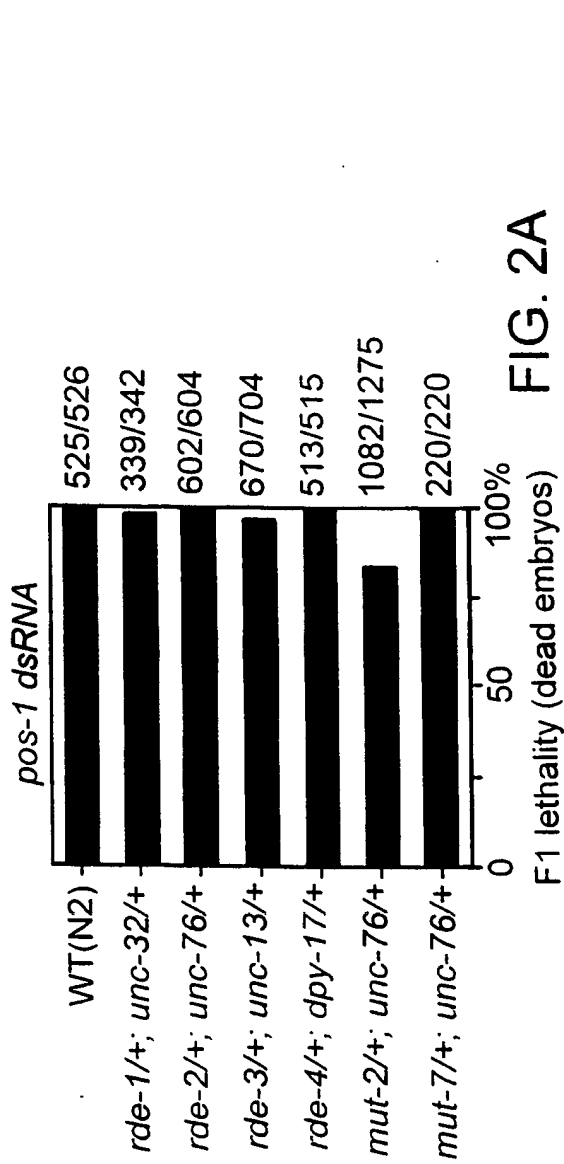


FIG. 1B



Title: RNA INTERFERENCE PATHWAY GENES AS TOOLS
FOR TARGETED GENETIC INTERFERENCE

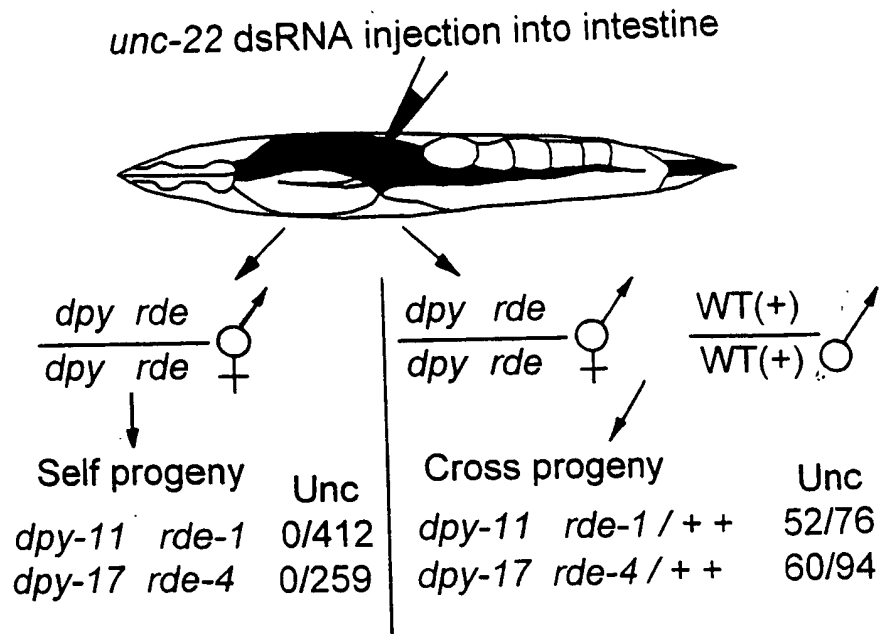


FIG. 3

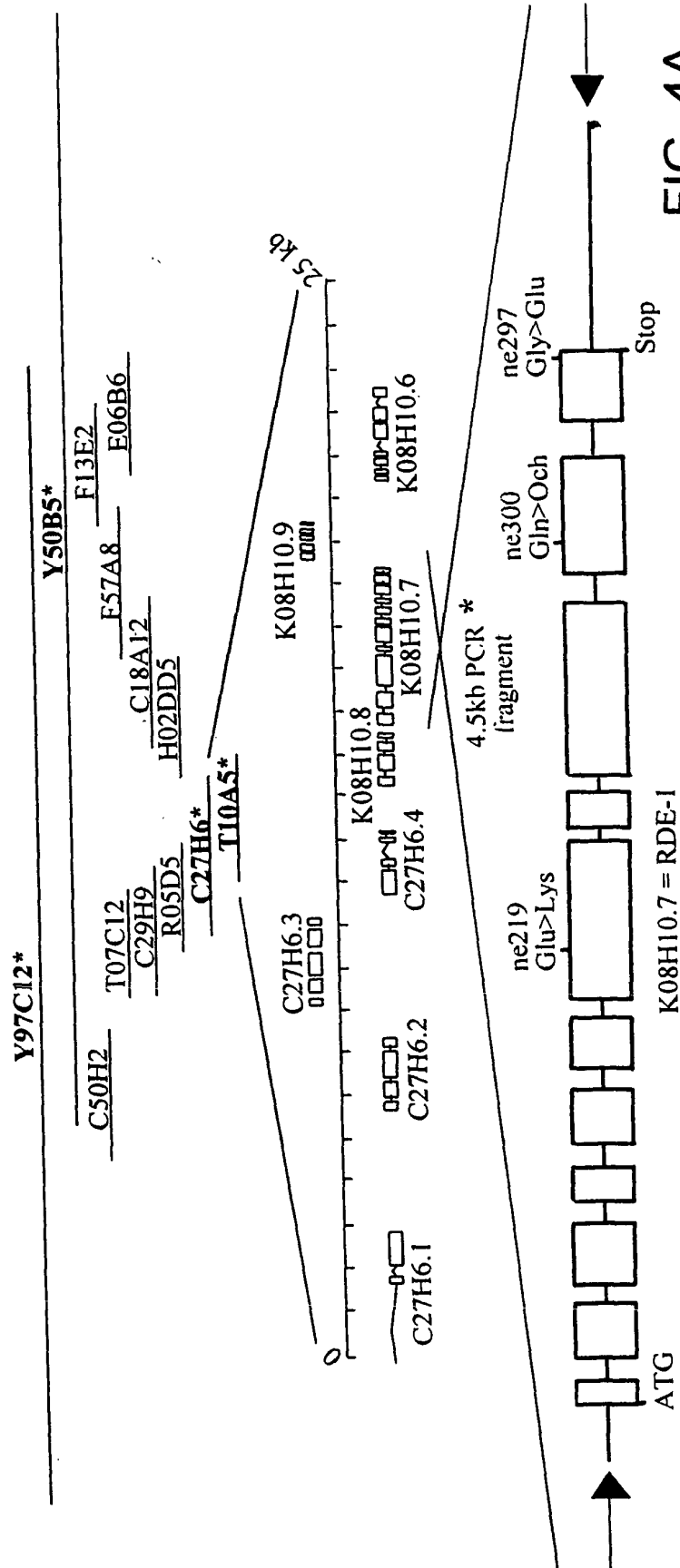


FIG. 4A

RDE-1	203	VN-----EEIKVQEA	AKNFVYDNN	SLRPESFHD	NRFES	QSEVAPRIE	AWEGII	IGIKEL	DGE	PVLN	-----
F48F7.1	235	S-----AVERQFS	SLKRW	GOVSIST	IEDA	VEGR	RO	DE	VA	QAM	VLIR
eIF2C	77	-----GKDRIFK	SVSKW	SCSIQA	HDAL	SCHLP	SV	PE	TI	QAD	VWIR
ZWILLE	226	-----GIINGPKR	RSYKAL	KEVARAN	MHH	GEFL	AG	KRAD	CE	QAY	QID
Sting	189	-----	RAGENIEIK	KA	VS	QSTDA	Q	Q	Q	VN	IL
RDE-1	267	-----FAIVDK	FYNAPK	MSLLD	YLL	IVDP	QSC	NDDV	VEK	DK	TKLM
F48F7.1	319	AGGAHS	AGQYHA	ESK	IGGGR	EVH	GFH	QSV	RP	Q	W
eIF2C	144	-----NE	LGGR	EVH	GFH	QSV	RP	Q	W	Q	W
ZWILLE	297	-----TEQRL	GEGL	SN	CG	YQ	SIR	PT	Q	MC	SL
Sting	244	-----	LENFR	MO	W	P	Q	Y	Q	T	S
RDE-1	336	VWDNEM	SRLTE	RHL	TFL	D	CE	NS	LV	Y	VT
F48F7.1	409	KIEITH	CGGOM	RK	GV	CV	NC	V	TR	PA	Q
eIF2C	220	KVEITH	CGGOM	RK	GV	CV	NC	V	TR	PA	Q
ZWILLE	372	KVEITH	CGGOM	RK	GV	CV	NC	V	TR	PA	Q
Sting	305	MGMVIL	TDYNNK	TR	IDD	VDF	Q	S	P	L	C
RDE-1	424	RYKNR	IDLV	MOD	KFL	KRA	TE	KPH	D	Y	K
F48F7.1	494	RCIRK	CLTD	V	Q	T	S	M	I	R	A
eIF2C	305	RCIRK	CLTD	V	Q	T	S	M	I	R	A
ZWILLE	454	RYTKR	NEK	Q	I	T	A	L	E	K	V
Sting	394	AMRAD	FRT	L	R	A	M	S	E	H	T

FIG. 4B-1

Title: RNA INTERFERENCE PATHWAY GENES AS TOOLS
FOR TARGETED GENETIC INTERFERENCE

```
RDE-1      514      QLNVVPEKELCCAVFVNE TAGNPCLENDVVKEYTELIGCKFRGIRIGANENRGAOSTMYDA TKNEAFYKNCITLNTGIGRFEIAATE
F48F7.1    581      RGRQFTTGDDRYWATACFAQ-QQHYKRENDLRFNFQRLQRI SRDAGVFIIVNEQFCCKAVSVEQVFNPAIYIQAQISG-----
eIF2C      392      RNKQFTTGDELRWATACFAP-DRQCTEVHKSETEELRKSRDAGVFIIVNEQFCCKAVSVEQVFNPAIYIQAQISG-----
ZWILLE     542      MNKKRMINGMTYSRWACVNFs---RSVOENVAGCECNEIGVCEVSGVEFNPEVITYSAREDSVEKALKHVYHTSMNKKTK-----
Sting      482      RTCSMFKNVHENRYVITPS-----RNLR--EQEEFVQXCIRTASSMKQNICNFIYEEIIPDDRNGTYSQAIDNANAN-----

RDE-1      604      AKQMFERLPDKQKVLMFIIISKRLQNAVGFVHYCDHTIGVANOCHISETVTKALASLRHEKSGKRIFYQIALKINAKLGGINQELDWS
F48F7.1    658      -----IQDVVYVLPG-KIPVYASVRVYCDHTIGVANOCHISETVTKALASLRHEKSGKRIFYQIALKINAKLGGINQELDWS
eIF2C      469      -----LQFVAVVLPFG-KIPVYASVRVYCDHTIGVANOCHISETVTKALASLRHEKSGKRIFYQIALKINAKLGGINQELDWS
ZWILLE     620      -----GKELELLALLPDNNGSLGDLKRIICEHEIGLISOCCLTRHVFKISK-----QYIADVSEIKINMKCGGRNTVIVDA
Sting      552      -----DPQIYVVMVRSNPNEEKVSCIKKKTCVDRFPFSQVVLKRVIAPRQQ-----KPTGLMSIATKVVIQMNAKLMGAP

RDE-1      694      EIAEISPEEKERKTMPLTMYVGIQDVTHPTSYSIDYSIAAVVASINPGGT-IYRNMIVTQEECRPGERAVAHGRE---RTDILEAKFVK
F48F7.1    725      V-----RPERENEVYVTHGCDITHPDAGDSRKPSTIAAVVCSIDAHPS-RVAATVRYVOCHROEITSEITY-----MYRE
eIF2C      536      G-----RSPVFOQPVYTHGADVTHPEAGDCKKPSIAAVVCSIDAHPN-RVCAWRYVOCHROEITSEITY-----MYRE
ZWILLE     691      IS-----CRILMSDIEPIIGADVTHPEAGDCKKPSIAAVVCSIDAHPN-RVCAWRYVOCHROEITSEITY-----MYRE
Sting      621      W-----QVVTPLHGLMVGEDVCHSP--KNKNKSYGAEVATMDQKESFRYFSTYNEHIKGOELISEQMSVN-----MAC
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FIG. 4B-2

Title: RNA INTERFERENCE PATHWAY GENES AS TOOLS
FOR TARGETED GENETIC INTERFERENCE

* ne300

780 LIREFAENNDNRAPAHIVAYRDGVSDSEMLRVSHDELRSKSEVKQFMSEKDEPEPKYTFIVIQKRHTRLLRRMEKDKPVNKKDLTP
F48F7.1 LLVQFYRNTR--KPAFIVAYRDGVSEGGTFNVLQDELRAKREAGAMIERGYQPG-----TFIVAQKRHTRLLRVNKKDQ--V-----
eIF2C LLHGFYKSTR--KPTRTVAYRDGVSEGGTFNVLQDELRAKREAGAMIERGYQPG-----TFIVAQKRHTRLLRCTEAGNER--V-----
ZWILLE LLISERKATG-QKPLRIIFAYRDGVSEGGTFNVLQDELRAKREAGAMIERGYQPG-----VTFIVAQKRHTRLLFANNHRDKNST-----
687 ALRSYQEQHR-SLPERIHIFRDGVGDGQLQVNSEVNTKDRLEIYKSAGKEGC-RMTEIISKRNISRYTGHNPV-----

870 AETDVAAAVKQWEEDMKEKETGIVNPSSGTTVDKILTVSKVKEDEFFLASHHGVLGTSRPGHYTVAYDDKGMQDEVIKMTYGLAFLSAR
F48F7.1 GRAYNPPGTTVDVGTTHPTTEDEFFLASHHGVLGTSRPGHYTVAYDDKGMQDEVIKMTYGLAFLSAR
eIF2C GRAYNPPGTTVDVGTTHPTTEDEFFLASHHGVLGTSRPGHYTVAYDDKGMQDEVIKMTYGLAFLSAR
ZWILLE DRSSNILEGTTVDVGTTHPTTEDEFFLASHHGVLGTSRPGHYTVAYDDKGMQDEVIKMTYGLAFLSAR
766 -----E-GTVDDVITLPEERYDFFLVSOAVRIGTVSPTSNNVISDNMGNA DKLOMESKMTHTMYN

E ne297

960 CRKPISLPVPVHYAHLSCCKAKELYRTYKEHYICDYAQPRTRHEMEHLFQTNVVKYPGMSFA----- (SEQ ID NO: 13)
F48F7.1 CTRSVSHPAPVYAHLVAFRARIHLVDRHDSCEGSGPSGTSEDTTLSNMAVAVQVILAEVLVSI----- (SEQ ID NO: 9)
eIF2C CTRSVSHPAPVYAHLVAFRARIHLVDRHDSCEGSGPSGTSEDTTLSNMAVAVQVILAEVLVSI----- (SEQ ID NO: 10)
ZWILLE CTRSVSVPVYAHLVAFRARIHLVDRHDSCEGSGPSGTSEDTTLSNMAVAVQVILAEVLVSI----- (SEQ ID NO: 6)
827 YSGTIRVPAVCHYAKLALVLSINRAPSAGLQNLQLYFL----- (SEQ ID NO: 7)

FIG. 4B-3

cagccacaagigatgaaacatgtctcgaatttcccgaaatgggaaaaaggattttatcgtcattctctcgatccggta
tgcacattattagcagctataagatatataagtttgatataataatataatgagatgaaatggcttgcgagggccacctg
gtaaatgcgacggcacaattctatgagaaagaaagtaactcttttggtaaatgggttcaagttctccagcaaaaatttacgat
cgggaatactacgagtatgaaagtgaaaaatgacaaaaggaaagtattgaaataagaaaaccagggaaaacctttcccaaaaaaag
agaaaattccaatgtagtgcttgtaaataggtcaaaactaatttttttcagtcgccgacgtgcgcaaaaactctcttggc
aacatcttcggcatgagaaagcagacagattttattctcgaaagactatgtttttgatgaaaaaggacactgttttatagt
gtttgtcgactgaaacactgtcacatcaaaaaatgctgggtttcggagaaagtagtaaaaaagggttcggagaaaaaaggatg
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atccggaaaaagacgaaagaaatcggaattacaattctcgaaggtttatgaaaaaacacgcattataacaacaa
ttagctttcagaatgttatgaccagaaagtctcgtaacgcttttggtaacgagggagattaagtgtaggttgcaata
ataataataataacaccctcaactcatttatatatatttaagacaattcggaaaaaattttgtgtacgataataatcaat

FIG. 5A

tctgcgagttcctgaatcggttcacgatccaaacagattcgaacaatcattagaagtagcaccaagaatcgaagcatggt
ttggaattacattggaatcaaagaattgttcgatgggtgaacctgtgtcctcaattttgcaagtaagtttgagaaactgcga
taaaaaatcatgtgatttttgtgaagttgtcgataaactattctacaatgcaccgaaaatgtctcttctggattatctt
ctcctaattgtcgacccccagtcgtgtaacgatgatgtacgaaaagatcttaaaacaaaactgatggcgggaaaaatgac
aatcagacaagccgcgcggccaagaattcgacaattattggaaaaattgaagctgaaatgcgcagaagttgggataac
aaatgtagtttaaattattcaacaattaatatacaaaattgattttcaggtcgagattgacagaacgacatctgacatt
tctagatttgtgcgaggaaaactctctgtttataaagtcactggtaaatcggacagaggaagaaatgcaaaaaagtacg
atactacattgttcaaaatctatgaggaaaacaaaaagttcattgagtttcccacctaccactagtcaaagttaaaagt
ggagcaaaagaatacgtgtaccaatggaacatcttgaagttcatgagaagccacaaagatacaagaatcgaattgatc
ggtagtgaagacaagtttctaaagcgagctacacgaaaacctcagactacaaagaaaataccctaaaaatgctgaaa
aattggatttctcttctgaagagctaaattttgtgaaagatttggattatgctcctcaacttcagatgatcgaatgtcca
ggaaagggttttgaagagccaatgcttgaatagtgttaatgaacaaattaaaatgacaccagtgattcgtggatttca
agaaaaacaattgaatgtggttccgaaaaagaactttgtgtgtctgtttttgtagtcaacgaaacagcgggaaatccat
gcttagaagagaacgacgttgtgtaagtgtttctacgtagattattccgaaatattttcagtaagttctacaccgaact
aattgggtggttgaagttccgtggaatacgaattggtgccaatgaaaacagaggagcgcaatctattatgtacgacgcga
cgaaaaatgaatatgccgtaagtttcagaaaaattgaaagtttttaaatatcatatttacagttctacaaaaattgtacac
taaataccggaatcggtagatttgaaatagccgcaacagaagcgaagaatatgtttgaacgttctccgataaagaaca
aaagtcttaatgttcattatcatttcaaacgacaactgaatgcttacgggtttgtgaaacattattgcgatcacaccat
cgggtgtagctaatecagcatattacttctgaaacagtcacaaaagctttggcatcactaaggcacgagaaaggatcaaaac
gaattttctatcaaattgcattgaaaatcaacgcgaaattaggaggtattaaccaggagcttgactggtcagaaattgca
gaaatatcaccagaagaaaaagaaagacggaaaaacaatgccattaactatgtatgttggaattgatgtaactcatccaa
ctcctacagtgggaattgattattctatagcggctgtagtagcgagratcaatccaggtggaactatctatcgaaatatga
ttgtgactcaagaagaatgtcgtcccggtgagcgtgcagtggtcatggacgggaaagaacagatatgttggaaagcaaa
ttcgtgaaattgctcagagaattcgcagaagtgaagttgtcttgagratttaaaagatctctgggatttttaattttttg

FIG. 5B

taaaccttcagaaacacgaatcgagcaccagcgcatattgtagtctatcgagacggagttagcggattcgggagatgcta
cgtgttagtcagtgaagcttcgacatctttaaaaaagcgaaagttaaaacaattcatctcggaacgggagatggagaaagatccagga
ggcggaaagtacacggttcattgtgattcagaaaaagacacaaatacacagattgcttcgaaagaatgggaaaaagataaagcccggtg
tcaataaaagatcttactcctgctgtaaacagatgtctcgctgttgcgtgcttaaacaaatggggaggaggtatgaaaaggaaaagc
aaagaaactgggaattgtgaacccatcatccggaaacaaactgtggataaaacttatcgttttcgaaaaatacaaaattcgattttt
cttggcatctcatgtgtgtctctgtgtacatctcgtccaggacattacacgtttatgtatgacgataaaagggaatgagcc
aagatgaaagtctatgtaagcgttttgaatagcaggttagcgatttttaggattttgtaatacgcgcatatagttattataaaaa
aatgtttcagaaaatgacctacggacttgcctttctctctgctagatgtcgaaaaacccatctcgttgccttccggttc
attatgctcatttatcatgtgaaaaaagcgaaagagctttatcgaaacttacaagggaacattacatcggtgactatgcacag
ccacggactcgacacgaaaatgggaacattttctccaaaactaacgtggaagtacccctgggaatgtcgttcgcataaacattttgc
aaaagtgtegcggttcaatacaaatcttcaattgtagatattgtactacttttttaaaagcccggttcaaaaatt
cattccatgactaacgttttcataaaattacttgaattt (SEQ ID NO:1)

FIG. 5C

CAGCCACAAAGTGATGAAAC- 5' UTR

1/1 31/11
ATG TCC TCG AAT TTT CCC GAA TTG GAA AAA GGA TTT TAT CGT CAT TCT CTC GAT CCG GAG
Met ser ser asn phe pro glu leu glu lys gly phe tyr arg his ser leu asp pro glu

61/21 91/31
ATG AAA TGG CTT GCG AGG CCC ACT GGT AAA TGC GAC GGC AAA TTC TAT GAG AAG AAA GTA
met lys trp leu ala arg pro thr gly lys cys asp gly lys phe tyr glu lys lys val

121/41 151/51
CTT CTT TTG GTA AAT TGG TTC AAG TTC TCC AGC AAA ATT TAC GAT CGG GAA TAC TAC GAG
leu leu leu val asn trp phe lys phe ser ser lys ile tyr asp arg glu tyr tyr glu

181/61 211/71
TAT GAA GTG AAA ATG ACA AAG GAA GTA TTG AAT AGA AAA CCA GGA AAA CCT TTC CCA AAA
tyr glu val lys met thr lys glu val leu asn arg lys pro gly lys pro phe pro lys

241/81 271/91
AAG ACA GAA ATT CCA ATT CCC GAT CGT GCA AAA CTC TTC TGG CAA CAT CTT CGG CAT GAG
lys thr glu ile pro ile pro asp arg ala lys leu phe trp gln his leu arg his glu

301/101 331/111
AAG AAG CAG ACA GAT TTT ATT CTC GAA GAC TAT GTT TTT GAT GAA AAG GAC ACT GTT TAT
lys lys gln thr asp phe ile leu glu asp tyr val phe asp glu lys asp thr val tyr

361/121 391/131
AGT GTT TGT CGA CTG AAC ACT GTC ACA TCA AAA ATG CTG GTT TCG GAG AAA GTA GTA AAA
ser val cys arg leu asn thr val thr ser lys met leu val ser glu lys val val lys

421/141 451/151
AAG GAT TCG GAG AAA AAA GAT GAA AAG GAT TTG GAG AAA AAA ATC TTA TAC ACA ATG ATA
lys asp ser glu lys lys asp glu lys asp leu glu lys lys ile leu tyr thr met ile

481/161 511/171
CTT ACC TAT CGT AAA AAA TTT CAC CTG AAC TTT AGT CGA GAA AAT CCG GAA AAA GAC GAA
leu thr tyr arg lys lys phe his leu asn phe ser arg glu asn pro glu lys asp glu

541/181 571/191
GAA GCG AAT CCG AGT TAC AAA TTC CTG AAG AAT GTT ATG ACC CAG AAA GTT CGC TAC GCG
glu ala asn arg ser tyr lys phe leu lys asn val met thr gln lys val arg tyr ala

601/201 631/211
CCT TTT GTG AAC GAG GAG ATT AAA GTA CAA TTC GCG AAA AAT TTT GTG TAC GAT AAT AAT
pro phe val asn glu glu ile lys val gln phe ala lys asn phe val tyr asp asn asn

661/221 691/231
TCA ATT CTG CGA GTT CCT GAA TCG TTT CAC GAT CCA AAC AGA TTC GAA CAA TCA TTA GAA
ser ile leu arg val pro glu ser phe his asp pro asn arg phe glu gln ser leu glu

721/241 751/251

FIG. 6A

37A GCA CCA AGA ATC GAA GCA TGG TTT GGA ATT TAC ATT GGA ATC AAA GAA TTG TTC GAT val ala pro arg ile glu ala trp phe gly ile tyr ile gly ile lys glu leu phe asp	
781/261	811/271
GGT GAA CCT GTG CTC AAT TTT GCA ATT GTC GAT AAA CTA TTC TAC AAT GCA CCG AAA ATG gly glu pro val leu asn phe ala ile val asp lys leu phe tyr asn ala pro lys met	
841/281	871/291
TCT CTT CTG GAT TAT CTT CTC CTA ATT GTC GAC CCC CAG TCG TGT AAC GAT GAT GTA CGA ser leu leu asp tyr leu leu leu ile val asp pro gln ser cys asn asp asp val arg	
901/301	931/311
AAA GAT CTT AAA ACA AAA CTG ATG GCG GGA AAA ATG ACA ATC AGA CAA GCC GCG CGG CCA lys asp leu lys thr lys leu met ala gly lys met thr ile arg gln ala ala arg pro	
961/321	991/331
AGA ATT CGA CAA TTA TTG GAA AAT TTG AAG CTG AAA TGC GCA GAA GTT TGG GAT AAC GAA arg ile arg gln leu leu glu asn leu lys leu lys cys ala glu val trp asp asn glu	
1021/341	1051/351
ATG TCG AGA TTG ACA GAA CGA CAT CTG ACA TTT CTA GAT TTG TGC GAG GAA AAC TCT CTT met ser arg leu thr glu arg his leu thr phe leu asp leu cys glu glu asn ser leu	
1081/361	1111/371
GTT TAT AAA GTC ACT GGT AAA TCG GAC AGA GGA AGA AAT GCA AAA AAG TAC GAT ACT ACA val tyr lys val thr gly lys ser asp arg gly arg asn ala lys lys ^a tyr asp thr thr	
1141/381	1171/391
TTG TTC AAA ATC TAT GAG GAA AAC AAA AAG TTC ATT GAG TTT CCC CAC CTA CCA CTA GTC leu phe lys ile tyr glu glu asn lys lys phe ile glu phe pro his leu pro leu val	
1201/401	1231/411
AAA GTT AAA AGT GGA GCA AAA GAA TAC GCT GTA CCA ATG GAA CAT CTT GAA GTT CAT GAG lys val lys ser gly ala lys glu tyr ala val pro met glu his leu glu val his glu	
1261/421	1291/431
AAG CCA CAA AGA TAC AAG AAT CGA ATT GAT CTG GTG ATG CAA GAC AAG TTT CTA AAG CGA lys pro gln arg tyr lys asn arg ile asp leu val met gln asp lys phe leu lys arg	
1321/441	1351/451
GCT ACA CGA AAA CCT CAC GAC TAC AAA GAA AAT ACC CTA AAA ATG CTG AAA GAA TTG GAT ala thr arg lys pro his asp tyr lys glu asn thr leu lys met leu lys glu leu asp	
1381/461	1411/471
TTC TCT TCT GAA GAG CTA AAT TTT GTT GAA AGA TTT GGA TTA TGC TCC AAA CTT CAG ATG phe ser ser glu glu leu asn phe val glu arg phe gly leu cys ser lys leu gln met	
1441/481	1471/491
ATC GAA TGT CCA GGA AAG GTT TTG AAA GAG CCA ATG CTT GTG AAT AGT GTA AAT GAA CAA ile glu cys pro gly lys val leu lys glu pro met leu val asn ser val asn glu gln	
1501/501	1531/511
ATT AAA ATG ACA CCA GTG ATT CGT GGA TTT CAA GAA AAA CAA TTG AAT GTG GTT CCC GAA ile lys met thr pro val ile arg gly phe gln glu lys gln leu asn val val pro glu	

FIG. 6B

1361/521	1391/531
AAA GAA GTT TGC TGT GGT GTT TTT GTA GTC AAC GAA ACA GCG GGA AAT CCA TGC TTA GAA	
lys glu leu cys cys ala val phe val val asn glu thr ala gly asn pro cys leu glu	
1421/541	1451/551
GAG AAC GAC GTT GTT AAG TTC TAC ACC GAA CTA ATT GGT GGT TGC AAG TTC CGT GGA ATA	
glu asn asp val val lys phe tyr thr glu leu ile gly gly cys lys phe arg gly ile	
1481/561	1711/571
CGA ATT GGT GCC AAT GAA AAC AGA GGA GCG CAA TCT ATT ATG TAC GAC GCG ACG AAA AAT	
arg ile gly ala asn glu asn arg gly ala gln ser ile met tyr asp ala thr lys asn	
1741/581	1771/591
GAA TAT GCC TTC TAC AAA AAT TGT ACA CTA AAT ACC GGA ATC GGT AGA TTT GAA ATA GCC	
glu tyr ala phe tyr lys asn cys thr leu asn thr gly ile gly arg phe glu ile ala	
1801/601	1831/611
GCA ACA GAA GCG AAG AAT ATG TTT GAA CGT CTT CCC GAT AAA GAA CAA AAA GTC TTA ATG	
ala thr glu ala lys asn met phe glu arg leu pro asp lys glu gln lys val leu met	
1861/621	1891/631
TTC ATT ATC ATT TCC AAA CGA CAA CTG AAT GCT TAC GGT TTT GTG AAA CAT TAT TGC GAT	
phe ile ile ile ser lys arg gln leu asn ala tyr gly phe val lys his tyr cys asp	
1921/641	1951/651
CAC ACC ATC GGT GTA GCT AAT CAG CAT ATT ACT TCT GAA ACA GTC ACA AAA GCT TTG GCA	
his thr ile gly val ala asn gln his ile thr ser glu thr val thr lys ala leu ala	
1981/661	2011/671
TCA CTA AGG CAC GAG AAA GGA TCA AAA CGA ATT TTC TAT CAA ATT GCA TTG AAA ATC AAC	
ser leu arg his glu lys gly ser lys arg ile phe tyr gln ile ala leu lys ile asn	
2041/681	2071/691
GCG AAA TTA GGA GGT ATT AAC CAG GAG CTT GAC TGG TCA GAA ATT GCA GAA ATA TCA CCA	
ala lys leu gly gly ile asn gln glu leu asp trp ser glu ile ala glu ile ser pro	
2101/701	2131/711
GAA GAA AAA GAA AGA CCG AAA ACA ATG CCA TTA ACT ATG TAT GTT GGA ATT GAT GTA ACT	
glu glu lys glu arg arg lys thr met pro leu thr met tyr val gly ile asp val thr	
2161/721	2191/731
CAT CCA ACC TCC TAC AGT GGA ATT GAT TAT TCT ATA GCG GCT GTA GTA GCG AGT ATC AAT	
his pro thr ser tyr ser gly ile asp tyr ser ile ala ala val val ala ser ile asn	
2221/741	2251/751
CCA GGT GGA ACT ATC TAT CGA AAT ATG ATT GTG ACT CAA GAA GAA TGT CGT CCC GGT GAG	
pro gly gly thr ile tyr arg asn met ile val thr gln glu glu cys arg pro gly glu	
2281/761	2311/771
CGT GCA GTG GCT CAT GGA CCG GAA AGA ACA GAT ATT TTG GAA GCA AAG TTC GTG AAA TTG	
arg ala val ala his gly arg glu arg thr asp ile leu glu ala lys phe val lys leu	
2341/781	2371/791
CTC AGA GAA TTC GCA GAA AAC AAC GAC AAT CGA GCA CCA GCG CAT ATT GTA GTC TAT CGA	
leu arg glu phe ala glu asn asn asp asn arg ala pro ala his ile val val tyr arg	

FIG. 6C

2401/801 2431/811
GAC GGA GTT AGC GAT TCG GAG ATG CTA CGT GTT AGT CAT GAT GAG CTT CGA TCT TTA AAA
asp gly val ser asp ser glu met leu arg val ser his asp glu leu arg ser leu lys

2461/821 2491/831
AGC GAA GTA AAA CAA TTC ATG TCG GAA CGG GAT GGA GAA GAT CCA GAG CCG AAG TAC ACG
ser glu val lys gln phe met ser glu arg asp gly glu asp pro glu pro lys tyr thr

2521/841 2551/851
TTC ATT GTG ATT CAG AAA AGA CAC AAT ACA CGA TTG CTT CGA AGA ATG GAA AAA GAT AAG
phe ile val ile gln lys arg his asn thr arg leu leu arg arg met glu lys asp lys

2581/861 2611/871
CCA GTG GTC AAT AAA GAT CTT ACT CCT GCT GAA ACA GAT GTC GCT GTT GCT GCT GTT AAA
pro val val asn lys asp leu thr pro ala glu thr asp val ala val ala ala val lys

2641/881 2671/891
CAA TGG GAG GAG GAT ATG AAA GAA AGC AAA GAA ACT GGA ATT GTG AAC CCA TCA TCC GGA
gln trp glu glu asp met lys glu ser lys glu thr gly ile val asn pro ser ser gly

2701/901 2731/911
ACA ACT GTG GAT AAA CTT ATC GTT TCG AAA TAC AAA TTC GAT TTT TTC TTG GCA TCT CAT
thr thr val asp lys leu ile val ser lys tyr lys phe asp phe phe leu ala ser his

2761/921 2791/931
CAT GGT GTC CTT GGT ACA TCT CGT CCA GGA CAT TAC ACT GTT ATG TAT GAC GAT AAA GGA
his gly val leu gly thr ser arg pro gly his tyr thr val met tyr asp asp lys gly

2821/941 2851/951
ATG AGC CAA GAT GAA GTC TAT AAA ATG ACC TAC GGA CTT GCT TTT CTC TCT GCT AGA TGT
met ser gln asp glu val tyr lys met thr tyr gly leu ala phe leu ser ala arg cys

2881/961 2911/971
CGA AAA CCC ATC TCG TTG CCT GTT CCG GTT CAT TAT GCT CAT TTA TCA TGT GAA AAA GCG
arg lys pro ile ser leu pro val pro val his tyr ala his leu ser cys glu lys ala

2941/981 2971/991
AAA GAG CTT TAT CGA ACT TAC AAG GAA CAT TAC ATC GGT GAC TAT GCA CAG CCA CGG ACT
lys glu leu tyr arg thr tyr lys glu his tyr ile gly asp tyr ala gln pro arg thr

3001/1001 3031/1011
CGA CAC GAA ATG GAA CAT TTT CTC CAA ACT AAC GTG AAG TAC CCT GGA ATG TCG TTC GCA
arg his glu met glu his phe leu gln thr asn val lys tyr pro gly met ser phe ala

3061/1021 3091/1031
TAA CAT TTT GCA AAA GTG TCG CCC GTT TCA ATC AAA TTT TTC AAT TGT AGA TAT TGT ACT
CCH (SEQ ID NO:3)

3121/1041 3151/1051
TAC TTT TTT TTA AAG CCC GGT TTC AAA AAT TCA TTC CAT GAC TAA CGT TTT CAT AAA TTA

3181/1061
CTT GAA ATT TAA AAA AAA AAA AAA AAA (SEQ ID NO:2)

FIG. 6D

Title: RNA INTERFERENCE PATHWAY GENES AS TOOLS
 FOR TARGETED GENETIC INTERFERENCE

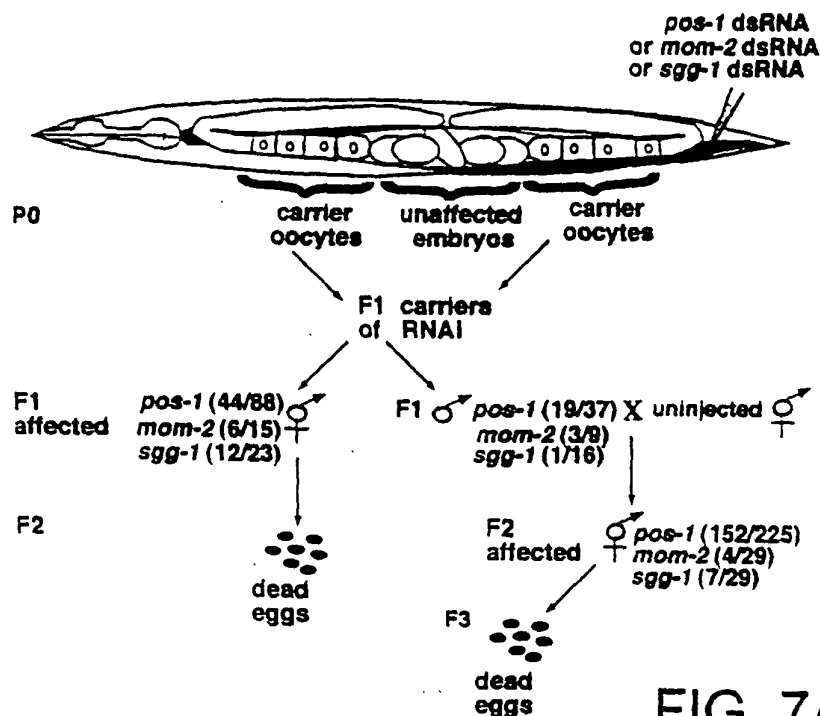


FIG. 7A

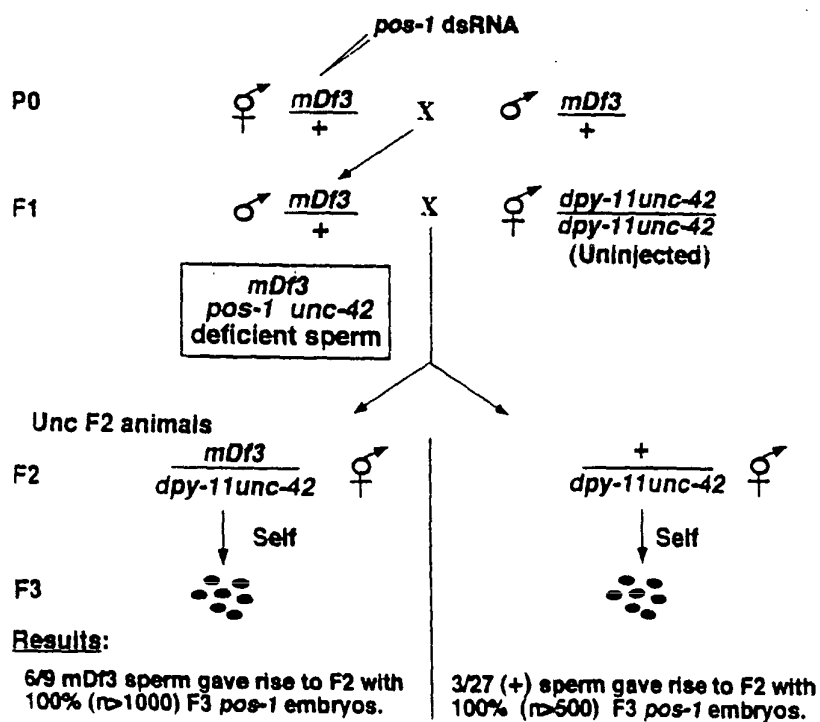


FIG. 7B





Injected P0	F1				
 $\frac{\text{pos-1 dsRNA} \text{ } rde-1 \text{ } unc-42}{+}$	$\xrightarrow{\text{self X}}$ <table> <tr> <td><i>rde-1</i> (-)</td> <td>11/24</td> </tr> <tr> <td><i>rde-1</i> (+)</td> <td>9/72</td> </tr> </table>	<i>rde-1</i> (-)	11/24	<i>rde-1</i> (+)	9/72
<i>rde-1</i> (-)	11/24				
<i>rde-1</i> (+)	9/72				
 $\frac{rde-2 \text{ } unc-13}{+}$	\longrightarrow <table> <tr> <td><i>rde-2</i> (-)</td> <td>0/39</td> </tr> <tr> <td><i>rde-2</i> (+)</td> <td>23/78</td> </tr> </table>	<i>rde-2</i> (-)	0/39	<i>rde-2</i> (+)	23/78
<i>rde-2</i> (-)	0/39				
<i>rde-2</i> (+)	23/78				
 $\frac{mut-7 \text{ } dpy-17}{+}$	\longrightarrow <table> <tr> <td><i>mut-7</i> (-)</td> <td>0/15</td> </tr> <tr> <td><i>mut-7</i> (+)</td> <td>20/50</td> </tr> </table>	<i>mut-7</i> (-)	0/15	<i>mut-7</i> (+)	20/50
<i>mut-7</i> (-)	0/15				
<i>mut-7</i> (+)	20/50				
 $\frac{rde-4 \text{ } unc-69}{+}$	\longrightarrow <table> <tr> <td><i>rde-4</i> (-)</td> <td>5/15</td> </tr> <tr> <td><i>rde-4</i> (+)</td> <td>11/48</td> </tr> </table>	<i>rde-4</i> (-)	5/15	<i>rde-4</i> (+)	11/48
<i>rde-4</i> (-)	5/15				
<i>rde-4</i> (+)	11/48				

FIG. 8A



P0	Injected F1		
 $\frac{rde-1 \text{ } unc-42}{+}$	$\xrightarrow{\text{pos-1 dsRNA}}$ <table> <tr> <td>$\frac{rde-1 \text{ } unc-42}{rde-1 \text{ } unc-42}$</td> <td>0/37</td> </tr> </table>	$\frac{rde-1 \text{ } unc-42}{rde-1 \text{ } unc-42}$	0/37
$\frac{rde-1 \text{ } unc-42}{rde-1 \text{ } unc-42}$	0/37		
 $\frac{rde-4 \text{ } unc-69}{+}$	$\xrightarrow{\text{pos-1 dsRNA}}$ <table> <tr> <td>$\frac{rde-4 \text{ } unc-69}{rde-4 \text{ } unc-69}$</td> <td>0/37</td> </tr> </table>	$\frac{rde-4 \text{ } unc-69}{rde-4 \text{ } unc-69}$	0/37
$\frac{rde-4 \text{ } unc-69}{rde-4 \text{ } unc-69}$	0/37		

FIG. 8B

Title: RNA INTERFERENCE PATHWAY GENES AS TOOLS
 FOR TARGETED GENETIC INTERFERENCE

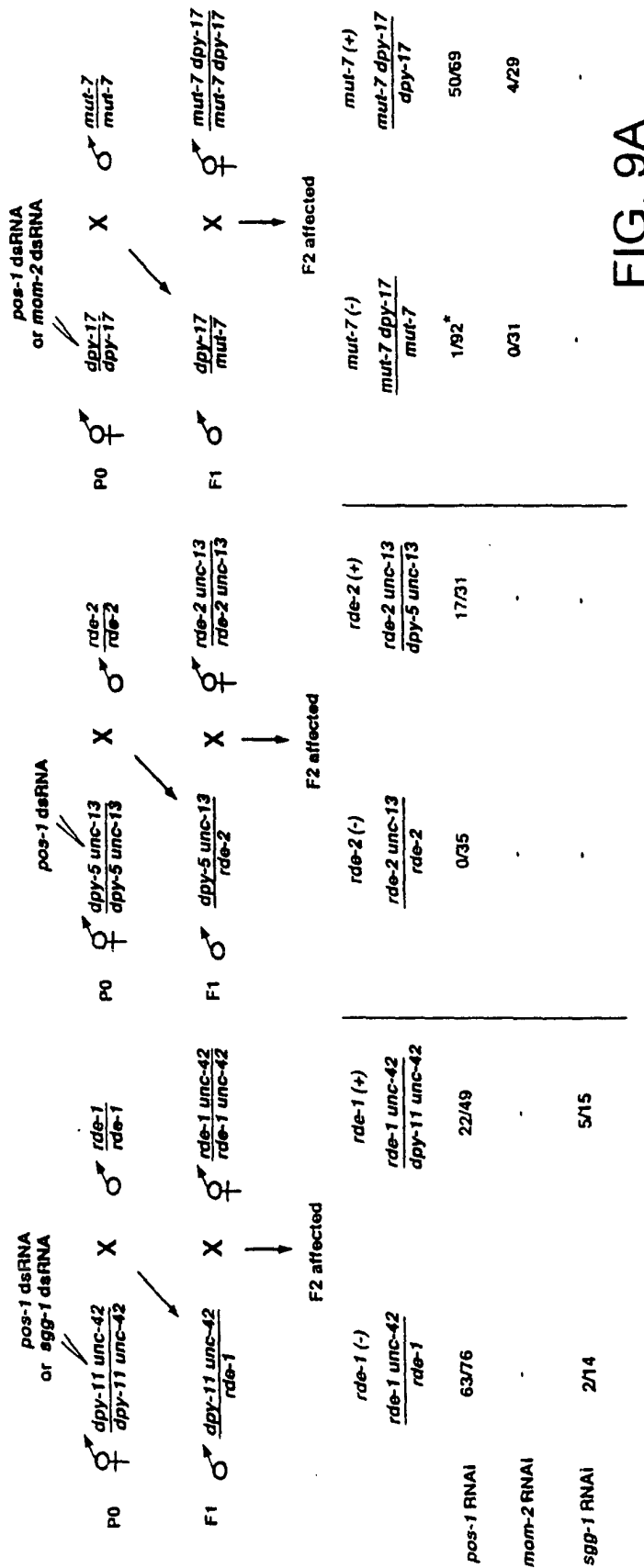


FIG. 9A

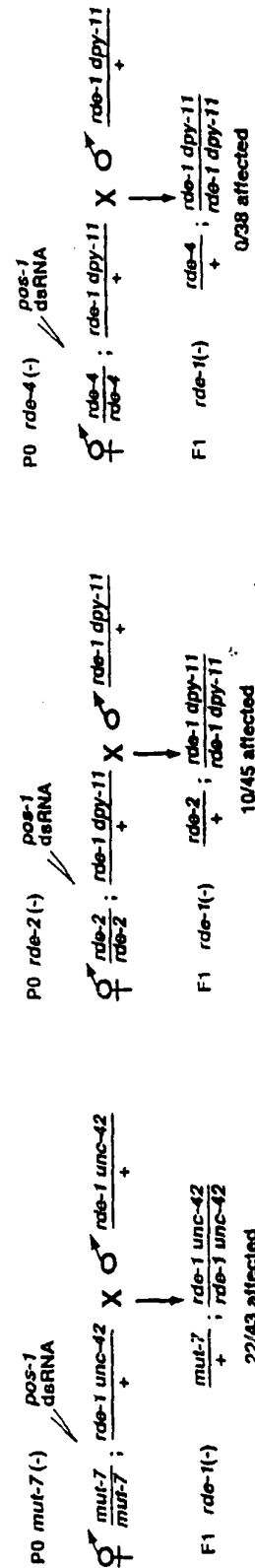


FIG. 9B

Title: RNA INTERFERENCE PATHWAY GENES AS TOOLS
FOR TARGETED GENETIC INTERFERENCE

10 20 30 40 50 60
ATGGATTTTAACCAAATAACGTTTGAAGCGTTTTCGGTGGATCAGATGTTTCTATGAAG
M D L T K L T F E S Y F G G S D V P M K

70 80 90 100 110 120
CCTTCCCGATCGGAGGATAACAAAACGCCAAGAAACAGAACAGATTTGGAGATGTTTCTG
P S R S E D N K T P R N R T D L E M F L

130 140 150 160 170 180
AAGAAACTCCCCTCATGGTACTAGAAGAGGCTGCTAAGGCTGTCTATCAAAAGACGCCA
K K T P L M V L E E A A K A V Y Q K T P

190 200 210 220 230 240
ACTTGGGGCACTGTGCAACTTCCTGAAGGCTTCGAGATGACGTTGATTCTGAATGAAATT
T W G T V E L P E G F E M T L I L N E I

250 260 270 280 290 300
ACTGTAAAAGGCCAGGCAACAAGCAAGAAAGCTGCGAGACAAAAGGCTGCTGTTGAATAT
T V K G Q A T S K K A A R Q K A A V E Y

310 320 330 340 350 360
TTACGCAAGGTTGTGGAGAAAGGAAAGCACGAAATCTTTTTTCATTCTGGAACAACCAAA
L R K V V E K G K H E I F F I P G T T K

370 380 390 400 410 420
GAAGAAGCTCTTTTGAATATTGATCAAATATCGGATAAGGCTGAGGAATTGAAACGATCA
E E A L S N I D Q I S D K A E E L K R S

430 440 450 460 470 480
ACTTCAGATGCTGTTTCAGGATAACGATAACGATGATTTCGATTCTACAAGTGCTGAATTT
T S D A V Q D N D N D D S I P T S A E F

490 500 510 520 530 540
CCACCTGGTATTTTCGCCAACCGAGAATTGGGTTCGGAAGTTGCAGGAAAAATCTCAAAA
P P G I S P T E N W V G K L Q E K S Q K

550 560 570 580 590 600
AGCAAGCTGCAAGCCCCAATCTATGAAGATTCCAAGAATGAGAGAACCGAGCGTTTCTTG
S K L Q A P I Y E D S K N E R T E R F L

610 620 630 640 650 660
GTTATATGCACGATGTGCAATCAAAAAACAGAGGAATCAGAAGTAAGAAGAAGGACGCA
V I C T M C N Q K T R G I R S K K K D A

670 680 690 700 710 720
AAGAATCTTGCAGCATGGTTGATGTGGAAAGCGTTGGAAGACGGTATCGAATCTCTGGAA
K N L A A W L M W K A L E D G I E S L E

730 740 750 760 770 780
TCATATGATATGGTTGATGTGATTGAAAATTTGGAAGAAGCTGAACATTTACTCGAAATT
S Y D M V D V I E N L E E A E H L L E I

FIG. 10A

```

      790      800      810      820      830      840
CAGGATCAAGCATCCAAGATTAAAGACAAGCATTCCGCACTGATTGATATACTCTCGGAC
Q D Q A S K I K D K H S A L I D I L S D

      850      860      870      880      890      900
AAGAAAAGATTTTCAGACTACAGCATGGATTTCAACGTATTATCAGTGAGCACAATGGGA
K K R F S D Y S M D F N V L S V S T M G

      910      920      930      940      950      960
ATACATCAGGTGCTATTGGAAATCTCGTTCCGGCGTCTAGTTTCTCCAGACCCCGACGAT
I H Q V L L E I S F R R L V S P D P D D

      970      980      990     1000     1010     1020
TTGGAAATGGGAGCAGAACACACCCAGACTGAAGAAATTATGAAGGCTACTGCCGAGAAG
L E M G A E H T Q T E E I M K A T A E K

     1030     1040     1050     1060     1070     1080
GAAAAGCTACGGAAGAAGAATATGCCAGATTCCGGGCGGCTAGTGTGCTGGACATGGT
E K L R K K N M P D S G P L V F A G H G

     1090     1100     1110     1120     1130     1140
TCATCGGCGGAAGAGGCTAAACAGTGTGCTTGTAATCGGCGATTATCCATTTCACACC
S S A E E A K Q C A C K S A I I H F N T

     1150     1160     1170     1180     1190     1200
TATGATTTTCACGGATTGAAAATATTATTGCGTATTCCTGAAAAATGAAGCGTCTGAATGA
Y D F T D * K Y Y C V F L K N E A S E *

     1210     1220     1230
TTATAAAAAAAAAAAAAAAAAAAAAA (SEQ ID NO:4)
L * K K K K K (SEQ ID NO:5)

```

FIG. 10B

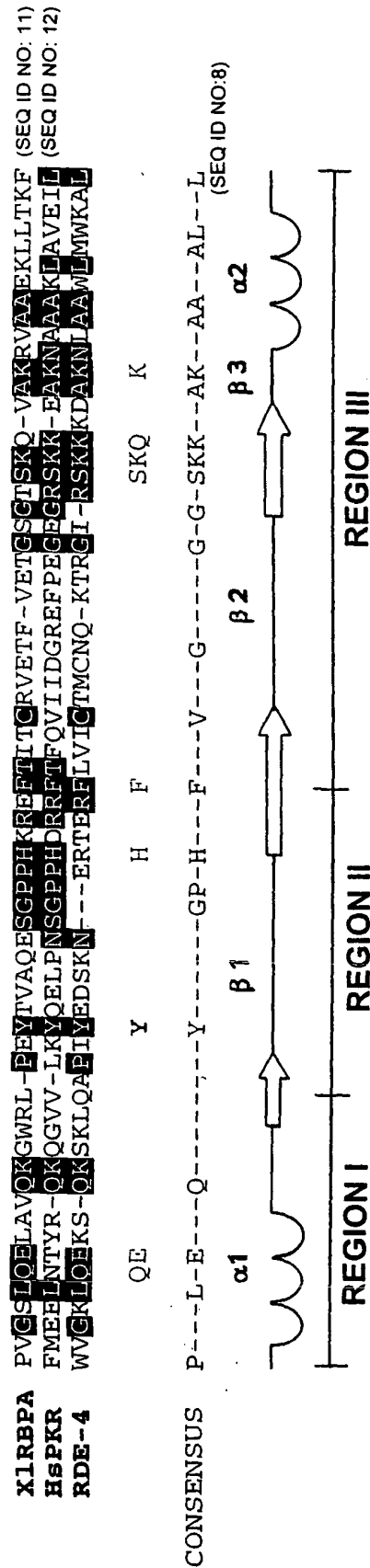


FIG. 11

FIG. 12 Rescue of *rde-4*:

